



SEQUENCE LISTING

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AHMED, NUZHAT

<120> A METHOD OF MODULATING INTEGRIN MEDIATED CELLULAR ACTIVITY
AND AGENTS USEFUL FOR SAME

<130> BLAKE-046XX

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<141> 2002-03-27

<150> PQ 1248

<151> 1999-06-28

<150> PQ 8003

<151> 2000-06-06

<160> 29

<170> PatentIn version 3.1

<210> 1

<211> 788

<212> PRT

<213> HOMO SAPIENS

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Met Gly Ile Glu Leu Leu Cys Leu Phe Phe Leu Phe Leu Gly Arg Asn
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Asp Ser Arg Thr Arg Trp Leu Cys Leu Gly Gly Ala Glu Thr Cys Glu
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Asp Cys Leu Leu Ile Gly Pro Gln Cys Ala Trp Cys Ala Gln Glu Asn
35 40 45

Phe Thr His Pro Ser Gly Val Gly Glu Arg Cys Asp Thr Pro Ala Asn
50 55 60

Leu Leu Ala Lys Gly Cys Gln Leu Asn Phe Ile Glu Asn Pro Val Ser
65 70 75 80

Gln Val Glu Ile Leu Lys Asn Lys Pro Leu Ser Val Gly Arg Gln Lys
85 90 95

Asn Ser Ser Asp Ile Val Gln Ile Ala Pro Gln Ser Leu Ile Leu Lys
100 105 110

Leu Arg Pro Gly Gly Ala Gln Thr Leu Gln Val His Val Arg Gln Thr
115 120 125

Glu Asp Tyr Pro Val Asp Leu Tyr Tyr Leu Met Asp Leu Ser Ala Ser
130 135 140

Met Asp Asp Asp Leu Asn Thr Ile Lys Glu Leu Gly Ser Gly Leu Ser
 145 150 155 160

Lys Glu Met Ser Lys Leu Thr Ser Asn Phe Arg Leu Gly Phe Gly Ser
 165 170 175

Phe Val Glu Lys Pro Val Ser Pro Phe Val Lys Thr Thr Pro Glu Glu
 180 185 190

Ile Ala Asn Pro Cys Ser Ser Ile Pro Tyr Phe Cys Leu Pro Thr Phe
 195 200 205

Gly Phe Lys His Ile Leu Pro Leu Thr Asn Asp Ala Glu Arg Phe Asn
 210 215 220

Glu Ile Val Lys Asn Gln Lys Ile Ser Ala Asn Ile Asp Thr Pro Glu
 225 230 235 240

Gly Gly Phe Asp Ala Ile Met Gln Ala Ala Val Cys Lys Glu Lys Ile
 245 250 255

Gly Trp Arg Asn Asp Ser Leu His Leu Leu Val Phe Val Ser Asp Ala
 260 265 270

Asp Ser His Phe Gly Met Asp Ser Lys Leu Ala Gly Ile Val Ile Pro
 275 280 285

Asn Asp Gly Leu Cys His Leu Asp Ser Lys Asn Glu Tyr Ser Met Ser
 290 295 300

Thr Val Leu Glu Tyr Pro Thr Ile Gly Gln Leu Ile Asp Lys Leu Val
 305 310 315 320

Gln Asn Asn Val Leu Leu Ile Phe Ala Val Thr Gln Glu Gln Val His
 325 330 335

Leu Tyr Glu Asn Tyr Ala Lys Leu Ile Pro Gly Ala Thr Val Gly Leu
 340 345 350

Leu Gln Lys Asp Ser Gly Asn Ile Leu Gln Leu Ile Ile Ser Ala Tyr
 355 360 365

Glu Glu Leu Arg Ser Glu Val Glu Leu Glu Val Leu Gly Asp Thr Glu
 370 375 380

Gly Leu Asn Leu Ser Phe Thr Ala Ile Cys Asn Asn Gly Thr Leu Phe
 385 390 395 400

Gln His Gln Lys Lys Cys Ser His Met Lys Val Gly Asp Thr Ala Ser
 405 410 415
 Phe Ser Val Thr Val Asn Ile Pro His Cys Glu Arg Arg Ser Arg His
 420 425 430
 Ile Ile Ile Lys Pro Val Gly Leu Gly Asp Ala Leu Glu Leu Leu Val
 435 440 445
 Ser Pro Glu Cys Asn Cys Asp Cys Gln Lys Glu Val Glu Val Asn Ser
 450 455 460
 Ser Lys Cys His His Gly Asn Gly Ser Phe Gln Cys Gly Val Cys Ala
 465 470 475 480
 Cys His Pro Gly His Met Gly Pro Arg Cys Glu Cys Gly Glu Asp Met
 485 490 495
 Leu Ser Thr Asp Ser Cys Lys Glu Ala Pro Asp His Pro Ser Cys Ser
 500 505 510
 Gly Arg Gly Asp Cys Tyr Cys Gly Gln Cys Ile Cys His Leu Ser Pro
 515 520 525
 Tyr Gly Asn Ile Tyr Gly Pro Tyr Cys Gln Cys Asp Asn Phe Ser Cys
 530 535 540
 Val Arg His Lys Gly Leu Leu Cys Gly Gly Asn Gly Asp Cys Asp Cys
 545 550 555 560
 Gly Glu Cys Val Cys Arg Ser Gly Trp Thr Gly Glu Tyr Cys Asn Cys
 565 570 575
 Thr Thr Ser Thr Asp Ser Cys Val Ser Glu Asp Gly Val Leu Cys Ser
 580 585 590
 Gly Arg Gly Asp Cys Val Cys Gly Lys Cys Val Cys Thr Asn Pro Gly
 595 600 605
 Ala Ser Gly Pro Thr Cys Glu Arg Cys Pro Thr Cys Gly Asp Pro Cys
 610 615 620
 Asn Ser Lys Arg Ser Cys Ile Glu Cys His Leu Ser Ala Ala Gly Gln
 625 630 635 640
 Ala Gly Glu Glu Cys Val Asp Lys Cys Lys Leu Ala Gly Ala Thr Ile
 645 650 655

Ser Glu Glu Glu Asp Phe Ser Lys Asp Gly Ser Val Ser Cys Ser Leu
660 665 670

Gln Gly Glu Asn Glu Cys Leu Ile Thr Phe Leu Ile Thr Thr Asp Asn
675 680 685

Glu Gly Lys Thr Ile Ile His Ser Ile Asn Glu Lys Asp Cys Pro Lys
690 695 700

Pro Pro Asn Ile Pro Met Ile Met Leu Gly Val Ser Leu Ala Thr Leu
705 710 715 720

Leu Ile Gly Val Val Leu Leu Cys Ile Trp Lys Leu Leu Val Ser Phe
725 730 735

His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
740 745 750

Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
755 760 765

Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
770 775 780

Ser Thr Asp Cys
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Arg Ser Lys Ala Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg
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Arg Ser Lys Ala Lys Asn Pro Leu Tyr Arg
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Arg Ser Lys Ala Lys
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Asn Pro Leu Tyr Arg
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His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys Glu Lys Met Asn Ala
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Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys Ser Ala Val Thr Thr
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Val Val Asn Pro Lys Tyr Glu Gly Lys
35 40

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Ser Asp Leu Arg Glu Tyr Arg Arg Phe Glu Lys Glu Lys Leu Lys Ser
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Gln Trp Asn Asn Asp Asn Pro Leu Phe Lys Ser Ala Thr Thr Thr Val
20 25 30

Met Asn Pro Lys Phe Ala Glu Ser
35 40

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His Asp Arg Lys Glu Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg Ala
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Lys Trp Asp Thr Ala Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr
20 25 30

Phe Thr Asn Ile Thr Tyr Arg Gly Thr
35 40

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His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
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Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
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Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
35 40 45

Ser Thr Asp Ser
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His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
1 5 10 15

Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
20 25 30

Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
35 40 45

Ser Thr Asp Cys
50

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His Asp Arg Lys Glu Val Ala Lys Phe Glu Ala Glu Arg Ser Lys Ala
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Lys Trp Gln Thr Gly Thr
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Arg Ser Lys Ala Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg Gly
1 5 10 15

Ser Thr Ser Thr
20

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Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr Phe Lys Asn Val Thr Tyr
1 5 10 15

Lys His Arg Glu
20

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Phe Lys Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu
1 5 10 15

Ser Thr Asp Ser
20

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Arg Ser Lys Ala Lys Trp Gln Thr Gly Thr
1 5 10

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Asn Pro Leu Tyr Arg Gly Ser Thr Ser Thr
1 5 10

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Trp Gln Thr Gly Thr Asn Pro Leu Tyr Arg
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Lys Phe Glu Ala Glu Arg Ser Lys Ala Lys
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Ala Glu Arg Ser Lys Ala Lys Trp Gln Thr Gly Thr Asn Pro Leu Tyr
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Arg Gly

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Pro Ile Tyr Lys
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Lys Glu Lys Leu Lys Ser Gln Trp Asn Asn Asp Asn Pro Leu Phe Lys
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Arg Ala Arg Ala Lys Trp Asp Thr Ala Asn Asn Pro Leu Tyr Lys
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Arg Ser Arg Ala Arg Tyr Glu Met Ala Ser Asn Pro Leu Tyr Arg
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Arg Thr Asp Leu Asp Ser Leu Arg Thr Tyr Thr Leu
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aggatagttc tgtttcctgc 20

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atcataggaa tatttgagg 20

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Trp Gln Thr Gly Thr
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Asn Val Thr Tyr Lys His Arg Glu Lys Gln Lys Val Asp Leu Ser
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Thr Asp Cys

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<400> 29

Glu Lys Gln Lys Val Asp Leu Ser Thr Asp Cys
1 5 10